

[illegible]

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Page 7

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XX FN EP767174-A1.
 XX PD 09 APR 1997.
 XX FE 26-SEP-1996; 96EP-0306397.
 XX PR 20-SEP-1996; 96JP-0269105.
 XX PR 26-SEP-1995; 95JP-027025.
 XX PR 29-DEC-1990; 96JP-0067434.
 XX PA (HAYB) HAYASHIMAWA SEIKICHIRO KANEKO.
 XX PI AKITA K., FUKUI M., FUKIMOTO M., NAKATA Y., TANABE T.
 XX WP1: 1997-205481/19.
 XX PT Human protein that induces interferon-gamma produ. in
 P1 immunocompetent cells - useful for adoptive immunotherapy of
 P1 tumours and as antitumoural agent etc.
 XX PS claim 8: Page 20; 26pp; English.
 XX CC The present sequence represents a novel protein from human cells which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antitumour agent for antitumour
 CC immunotherapy, an artificial (including anti-AIDS) or antitumour agent,
 CC and in the treatment of atopic or immune system diseases, e.g., asthma,
 CC hay fever or eczema. When formulated with interleukin-4, it is used
 CC to treat leukaemia and thrombocytopaenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
 CC antitumour immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX SV Sequence 157 AA.
 XX Query Match 99.4% Score 811; LB 18; Length 157;
 XX Batch Local Similarity 99.4% Pred. No. 2,66,846
 XX Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX QY 1 VYVLEKLVNRLRRLRQVLTGKNEETFEATGEGEERARERETTSYKSGSGPM 60
 XX LB 1 YVVKLSKSVIRLNDPILIDPILPLIDMDSDSDSDSDPILIDSDKSDSPRM 60
 XX QY 61 AVTISVGVKSTSTSTFHL228 FVGNVGNKGNKQVIL205VLEPKKQVSTGSSV 120
 XX LB 61 APTISVGVKSTSTSTFHL228 FVGNVGNKGNKQVIL205VLEPKKQVSTGSSV 120
 XX QY 121 EYVLAETKEFTEELIEEELDEGEMVYSEL 157
 XX LB 121 EYVLAETKEFTEELIEEELDEGEMVYSEL 157
 XX RESULT 12
 XX W24258
 XX W24258 standard; Protein; 157 AA.
 XX AC W24258;
 XX XX
 XX D1 15-oct 1997 (first entry)
 XX XX
 XX DE Human protein for induction of interferon-gamma.
 XX XX
 XX KW Interferon-gamma; immunocompetent cells; malignant tumour;
 XX KW vital disease; factor for infection; immune disease;
 XX OS Homo sapiens.
 XX XX

XX FH Key Location/Qualifiers
 XX FT Misc difference 78 /note "Revised by AY1"
 XX FI
 XX XX JP09157180-A.
 XX XX 17 JUN 1997.
 XX XX 24 JAN 1996; 96JP 0028722.
 XX XX 04 OCT-1995; 95JP 0279006.
 XX XX 10 MAR 1995; 95JP 0278457.
 XX XX 29-SEP-1995; 95JP-0274988.
 XX XX (HAYB) HAYASHIMAWA SEIKICHIRO KANEKO.
 XX XX WP1: 1997-003991/34.
 XX XX N-PSDB; 080209.
 XX XX A drug combination including which induces interferon-gamma
 XX XX ascorol for treatment of malignant tumours, viral, bacterial or
 XX XX immune diseases.
 XX XX claim 1: Page 9; 14pp; unknown.
 XX XX This sequence represents a protein which induces interferon-gamma
 XX XX production in immunocompetent cells. This protein may be used as
 XX XX the major component in a drug for the prevention and treatment of
 XX XX viral, bacterial tumours, viral diseases, infection, infectious and
 XX XX immune diseases.
 XX SV Sequence 157 AA.
 XX Query Match 99.4% Score 811; LB 18; Length 157;
 XX Batch Local Similarity 99.4% Pred. No. 2,66,846
 XX Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX QY 1 VYVLEKLVNRLRRLRQVLTGKNEETFEATGEGEERARERETTSYKSGSGPM 60
 XX LB 1 YVVKLSKSVIRLNDPILIDPILPLIDMDSDSDSDSDPILIDSDKSDSPRM 60
 XX QY 61 AVTISVGVKSTSTSTFHL228 FVGNVGNKGNKQVIL205VLEPKKQVSTGSSV 120
 XX LB 61 APTISVGVKSTSTSTFHL228 FVGNVGNKGNKQVIL205VLEPKKQVSTGSSV 120
 XX QY 121 EYVLAETKEFTEELIEEELDEGEMVYSEL 157
 XX LB 121 EYVLAETKEFTEELIEEELDEGEMVYSEL 157
 XX RESULT 13
 XX W27158
 XX W27158 standard; Protein; 157 AA.
 XX AC W27158;
 XX XX
 XX D1 26 Nov 1998 (first entry)
 XX XX
 XX DE Human Interleukin 18 protein (IL-18).
 XX XX
 XX KW Human Interleukin 18 protein; IL-18; cytokine signal transduction;
 XX KW immune system; treatment; antitumour; allergic disease;
 XX KW immunosuppression;
 XX OS Homo sapiens.
 XX XX
 XX FH Key Location/Qualifiers
 XX FI Misc difference 73 /note "Revised by AY1"
 XX FI
 XX XX EP064785-A1.
 XX XX


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14 07-JUL-1998 (first entry)
XX
XX IFN-gamma inducing active protein.
XX
XX Interferon-gamma inducing precursor polypeptide (IFN-gamma);
XX Interferon-gamma inducing precursor polypeptide (IFN-gamma); killer cell
XX antiviral agent; antitumor agent; immunopotentiator; antiseptic.
XX
XX Mammalian.
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 78
XX /Label: 1to, 1th
XX
XX FRK210-5-AZ.
XX
XX 28-JAN-1998.
XX
XX 18-JUL-1997: 97EP-0305376.
XX
XX 31-JAN-1997: 97JP-0631374.
XX 25-JUL-1996: 96JP-0213267.
XX
XX (HAYASHI) HAYASHIYAKA SEIJIHISU KAZAKU.
XX
XX Kurimoto M, Tanimoto T.
XX
XX WP: 1998-08847/09.
XX N-PSDB: V18926.
XX
XX Conversion of Interferon Inducing Polypeptide Precursor to active
XX polypeptide: comprises use of Interferon-1 beta-converting enzyme
XX used for, e.g. enhancing cytotoxicity by killer cells
XX
XX
XX Claim 5: Page 15: 1pp: English.
XX
XX This is the amino acid sequence for the interferon gamma (IFN-gamma)
XX inducing active protein which is cleaved to form the active mature
XX protein when it is in contact with Interferon-1 beta-converting
XX enzyme (ICE). The polypeptide is used for inducing, e.g. production
XX of IFN-gamma a useful biologically active substance, enhancing
XX cytotoxicity by, and inducing the formation of killer cells. The
XX polypeptide may potentially be used as an antiviral, antitumor and
XX immunopotentiator and as an antiseptic.
XX
XX Sequence 157 AA:

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Query Match: 99.48; Score 811; 14 19; Length 157;
Best Local Similarity: 99.48; Prot. No. 2,46-843;
Matches 156; Conservative 0; Mismatches 1; Gaps 0;
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DB 1 YPKLESKTSVPRNENVILNENRFLPEPMNGLQVQVARETFLISNYGNGPEEN 60
GY 61 AVTLNKKKLSSTENKLSSTKIMPEENKLSKLSIFKSSVPEHMRQPFSSY 120
DB 61 AVTLNKKKLSSTENKLSSTKIMPEENKLSKLSIFKSSVPEHMRQPFSSY 120
GY 121 EGVYATKREKLEKLLKREHGLKSTIMYVQND 157
DB 121 EGVYATKREKLEKLLKREHGLKSTIMYVQND 157

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Search completed: May 11, 2001, 16:37:20
Job time: 37 sec



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1. A. 1000 0301 1004

2. A. 1000 0301 1004

3. A. 1000 0301 1004

4. A. 1000 0301 1004

5. A. 1000 0301 1004

6. A. 1000 0301 1004

7. A. 1000 0301 1004

8. A. 1000 0301 1004

9. A. 1000 0301 1004

10. A. 1000 0301 1004

11. A. 1000 0301 1004

12. A. 1000 0301 1004

13. A. 1000 0301 1004

14. A. 1000 0301 1004

15. A. 1000 0301 1004

16. A. 1000 0301 1004

17. A. 1000 0301 1004

18. A. 1000 0301 1004

19. A. 1000 0301 1004

20. A. 1000 0301 1004

21. A. 1000 0301 1004

22. A. 1000 0301 1004

23. A. 1000 0301 1004

24. A. 1000 0301 1004

25. A. 1000 0301 1004

26. A. 1000 0301 1004

27. A. 1000 0301 1004

28. A. 1000 0301 1004

29. A. 1000 0301 1004

30. A. 1000 0301 1004

31. A. 1000 0301 1004

32. A. 1000 0301 1004

33. A. 1000 0301 1004

34. A. 1000 0301 1004

35. A. 1000 0301 1004

36. A. 1000 0301 1004

37. A. 1000 0301 1004

38. A. 1000 0301 1004

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THE PROCESSION SOCIETY, 1810-1820

Run On: May 11, 2001, 16:46:44 ; Search time 13.78 seconds

THE UNIVERSITY OF CHICAGO PRESS

$$T_{\alpha}^{\beta} = (g_{\alpha\gamma} - (g_{\alpha\gamma} - g_{\beta\gamma})\delta_{\alpha\beta})\delta_{\beta\gamma} = g_{\alpha\beta}$$

Содержание: ТЕОРЕТИЧЕСКИЕ И МЕТОДИЧЕСКИЕ ОСНОВЫ ИЗУЧЕНИЯ ИСТОРИИ ИСТОРИКО-ПЕДАГОГИЧЕСКОГО НАУЧНОГО МЕТОДА 157

$$S^1 \times \mathbb{R}^2 \rightarrow \mathbb{R}^2 \quad (x, y) \mapsto (x^2 + y^2, xy)$$

Inflow 10.0, Output 6.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 94457

Minimum DB seq length: 0

Maximum job seq length: 2000000000

[illegible]

Listed first 45 summaries

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Database : *
Ministro_39: *

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

SUMMARY						
Result	No.	Score	Query Match	Query Length	ID	Description
1	816	100.0	193	1	1118_HUMAN	Q04116 Hemato sapiens
2	664	81.4	193	1	1118_HOSE	Q08847 Equus caballus
3	642	78.7	192	1	1118_PIG	Q13074 Sus scrofa
4	618	75.7	193	1	1118_CAMEA	Q98810 Camelus dromedarius
5	528	61.7	192	1	1118_MOUSE	U70386 Mus musculus
6	519.5	61.7	194	1	1118_RAT	U70360 Rattus norvegicus
7	81.5	10.0	266	1	1118_PIG	U70360 Rattus norvegicus
8	81	9.9	267	1	1118_RHIT	Q04822 Drosophila
9	80.5	9.9	1663	1	Q08_MOUSE	P01022 Mus musculus
10	79	9.7	1772	1	MSL_PLAYO	P11629 Plasmodium
11	77.5	9.5	270	1	1118_HOSE	Q26380 Equus caballus
12	75.4	9.4	192	1	1118_HOSE	Q26380 Equus caballus
13	74	9.2	167	1	MYO6_MOUSE	U70374 Mus musculus
14	73.4	9.1	351	1	PEP1_TENEA	U70374 Mus musculus
15	74.5	9.1	1036	1	Y414_MOUSE	U70374 Mus musculus
16	74.5	9.1	1228	1	PEP1_MOUSE	U70374 Mus musculus
17	74	9.1	279	1	1118_PLAYO	U70374 Mus musculus
18	74	9.1	2663	1	CEH2_HUMAN	Q042224 Homo sapiens
19	73	8.9	4790	1	FAM10_HUMAN	Q134717 Homo sapiens
20	72.5	8.5	268	1	1118_PLAYO	P01022 Mus musculus
21	72.5	8.2	467	1	MYO6_MOUSE	U70374 Mus musculus
22	72	8.8	708	1	PEP1_MOUSE	U70374 Mus musculus
23	72	8.6	859	1	KIN1_YEAST	Q04043 Drosophila
24	71.5	8.6	266	1	1118_MOUSE	U70374 Mus musculus
25	71.5	8.6	175	1	PEP1_MOUSE	U70374 Mus musculus
26	71.5	8.8	477	1	MYO6_MOUSE	U70374 Mus musculus
27	71.5	8.2	575	1	PEP1_MOUSE	U70374 Mus musculus
28	71	8.7	198	1	Y414_MOUSE	U70374 Mus musculus
29	70.5	8.6	268	1	1118_MOUSE	U70374 Mus musculus
30	70.5	8.6	764	1	MYO6_MOUSE	U70374 Mus musculus
31	70.5	8.6	1091	1	1118_MOUSE	U70374 Mus musculus
32	70.5	8.6	1230	1	MYO6_MOUSE	U70374 Mus musculus
33	70	8.6	451	1	MYO6_MOUSE	U70374 Mus musculus

[illegible]

1. The following information was obtained from the analysis of the sample submitted for analysis on May 11, 2001. The sample was identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The known compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The unknown compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The analysis was performed using the following methods: 1. Gas chromatography-mass spectrometry (GC-MS). 2. Infrared spectroscopy (IR). 3. Nuclear magnetic resonance spectroscopy (NMR). 4. X-ray fluorescence spectroscopy (XRF). 5. Atomic absorption spectroscopy (AAS). 6. Inductively coupled plasma-mass spectrometry (ICP-MS). 7. High-resolution mass spectrometry (HRMS). 8. Gel permeation chromatography (GPC). 9. Size exclusion chromatography (SEC). 10. Thin layer chromatography (TLC). 11. Paper chromatography. 12. Column chromatography. 13. Distillation. 14. Extraction. 15. Precipitation. 16. Crystallization. 17. Sublimation. 18. Evaporation. 19. Drying. 20. Storage. 21. Transport. 22. Packaging. 23. Labeling. 24. Documentation. 25. Reporting. 26. Archiving. 27. Retrieval. 28. Destruction. 29. Recycling. 30. Disposal. 31. Environmental impact. 32. Safety. 33. Health. 34. Toxicology. 35. Pharmacology. 36. Biophysics. 37. Biochemistry. 38. Molecular biology. 39. Cell biology. 40. Developmental biology. 41. Evolutionary biology. 42. Systematics. 43. Paleontology. 44. Geology. 45. Meteorology. 46. Oceanography. 47. Atmospheric science. 48. Earth and planetary science. 49. Space science. 50. Interdisciplinary research. 51. Transdisciplinary research. 52. Multidisciplinary research. 53. Cross-disciplinary research. 54. Collaborative research. 55. Open science. 56. Citizen science. 57. Participatory science. 58. Community science. 59. Public science. 60. Open access. 61. Creative Commons. 62. Public domain. 63. Copyright. 64. Patents. 65. Trademarks. 66. Intellectual property. 67. Data management. 68. Data sharing. 69. Data preservation. 70. Data archiving. 71. Data mining. 72. Data visualization. 73. Data analysis. 74. Data interpretation. 75. Data communication. 76. Data dissemination. 77. Data dissemination. 78. Data dissemination. 79. Data dissemination. 80. Data dissemination. 81. Data dissemination. 82. Data dissemination. 83. Data dissemination. 84. Data dissemination. 85. Data dissemination. 86. Data dissemination. 87. Data dissemination. 88. Data dissemination. 89. Data dissemination. 90. Data dissemination. 91. Data dissemination. 92. Data dissemination. 93. Data dissemination. 94. Data dissemination. 95. Data dissemination. 96. Data dissemination. 97. Data dissemination. 98. Data dissemination. 99. Data dissemination. 100. Data dissemination.

1. The following information was obtained from the analysis of the sample submitted for analysis on May 11, 2001. The sample was identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The known compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The unknown compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The analysis was performed using the following methods: 1. Gas chromatography-mass spectrometry (GC-MS). 2. Infrared spectroscopy (IR). 3. Nuclear magnetic resonance spectroscopy (NMR). 4. X-ray fluorescence spectroscopy (XRF). 5. Atomic absorption spectroscopy (AAS). 6. Inductively coupled plasma-mass spectrometry (ICP-MS). 7. High-resolution mass spectrometry (HRMS). 8. Gel permeation chromatography (GPC). 9. Size exclusion chromatography (SEC). 10. Thin layer chromatography (TLC). 11. Paper chromatography. 12. Column chromatography. 13. Distillation. 14. Extraction. 15. Precipitation. 16. Crystallization. 17. Sublimation. 18. Evaporation. 19. Drying. 20. Storage. 21. Transport. 22. Packaging. 23. Labeling. 24. Documentation. 25. Reporting. 26. Archiving. 27. Retrieval. 28. Destruction. 29. Recycling. 30. Disposal. 31. Environmental impact. 32. Safety. 33. Health. 34. Toxicology. 35. Pharmacology. 36. Biophysics. 37. Biochemistry. 38. Molecular biology. 39. Cell biology. 40. Developmental biology. 41. Evolutionary biology. 42. Systematics. 43. Paleontology. 44. Geology. 45. Meteorology. 46. Oceanography. 47. Atmospheric science. 48. Earth and planetary science. 49. Space science. 50. Interdisciplinary research. 51. Transdisciplinary research. 52. Multidisciplinary research. 53. Cross-disciplinary research. 54. Collaborative research. 55. Open science. 56. Citizen science. 57. Participatory science. 58. Community science. 59. Public science. 60. Open access. 61. Creative Commons. 62. Public domain. 63. Copyright. 64. Patents. 65. Trademarks. 66. Intellectual property. 67. Data management. 68. Data sharing. 69. Data preservation. 70. Data archiving. 71. Data mining. 72. Data visualization. 73. Data analysis. 74. Data interpretation. 75. Data communication. 76. Data dissemination. 77. Data dissemination. 78. Data dissemination. 79. Data dissemination. 80. Data dissemination. 81. Data dissemination. 82. Data dissemination. 83. Data dissemination. 84. Data dissemination. 85. Data dissemination. 86. Data dissemination. 87. Data dissemination. 88. Data dissemination. 89. Data dissemination. 90. Data dissemination. 91. Data dissemination. 92. Data dissemination. 93. Data dissemination. 94. Data dissemination. 95. Data dissemination. 96. Data dissemination. 97. Data dissemination. 98. Data dissemination. 99. Data dissemination. 100. Data dissemination.

1. The following information was obtained from the analysis of the sample submitted for analysis on May 11, 2001. The sample was identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The known compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The unknown compound is identified as a mixture of two substances, one of which is a known compound and the other is an unknown compound. The analysis was performed using the following methods: 1. Gas chromatography-mass spectrometry (GC-MS). 2. Infrared spectroscopy (IR). 3. Nuclear magnetic resonance spectroscopy (NMR). 4. X-ray fluorescence spectroscopy (XRF). 5. Atomic absorption spectroscopy (AAS). 6. Inductively coupled plasma-mass spectrometry (ICP-MS). 7. High-resolution mass spectrometry (HRMS). 8. Gel permeation chromatography (GPC). 9. Size exclusion chromatography (SEC). 10. Thin layer chromatography (TLC). 11. Paper chromatography. 12. Column chromatography. 13. Distillation. 14. Extraction. 15. Precipitation. 16. Crystallization. 17. Sublimation. 18. Evaporation. 19. Drying. 20. Storage. 21. Transport. 22. Packaging. 23. Labeling. 24. Documentation. 25. Reporting. 26. Archiving. 27. Retrieval. 28. Destruction. 29. Recycling. 30. Disposal. 31. Environmental impact. 32. Safety. 33. Health. 34. Toxicology. 35. Pharmacology. 36. Biophysics. 37. Biochemistry. 38. Molecular biology. 39. Cell biology. 40. Developmental biology. 41. Evolutionary biology. 42. Systematics. 43. Paleontology. 44. Geology. 45. Meteorology. 46. Oceanography. 47. Atmospheric science. 48. Earth and planetary science. 49. Space science. 50. Interdisciplinary research. 51. Transdisciplinary research. 52. Multidisciplinary research. 53. Cross-disciplinary research. 54. Collaborative research. 55. Open science. 56. Citizen science. 57. Participatory science. 58. Community science. 59. Public science. 60. Open access. 61. Creative Commons. 62. Public domain. 63. Copyright. 64. Patents. 65. Trademarks. 66. Intellectual property. 67. Data management. 68. Data sharing. 69. Data preservation. 70. Data archiving. 71. Data mining. 72. Data visualization. 73. Data analysis. 74. Data interpretation. 75. Data communication. 76. Data dissemination. 77. Data dissemination. 78. Data dissemination. 79. Data dissemination. 80. Data dissemination. 81. Data dissemination. 82. Data dissemination. 83. Data dissemination. 84. Data dissemination. 85. Data dissemination. 86. Data dissemination. 87. Data dissemination. 88. Data dissemination. 89. Data dissemination. 90. Data dissemination. 91. Data dissemination. 92. Data dissemination. 93. Data dissemination. 94. Data dissemination. 95. Data dissemination. 96. Data dissemination. 97. Data dissemination. 98. Data dissemination. 99. Data dissemination. 100. Data dissemination.

Protein biosynthesis,
KM 40194 MW: 699.836P883B5.770 2806.4
SD SEQUENCE 451 AA:

Fri May 11 16:44:19 2001

us-09-030-061-6.rsp

Page 10

4.2. REVERSE TRANSCRIPTION-PCR AMPLIFICATION OF THE 3' END OF THE 28S rRNA

2.1. MATERIALS AND METHODS

2.1.1. RNA Extraction and Purification

2.1.2. Reverse Transcription-PCR

2.1.3. Gel Electrophoresis and DNA Sequencing

2.1.4. Sequence Analysis

2.1.5. Phylogenetic Analysis

2.1.6. Statistical Analysis

2.1.7. Results and Discussion

2.1.8. Conclusions

2.1.9. Acknowledgments

2.1.10. References

2.1.11. Appendix

2.1.12. Figures

2.1.13. Tables

2.1.14. Glossary

2.1.15. Index

2.1.16. Bibliography

2.1.17. Appendix

2.1.18. Figures

2.1.19. Tables

2.1.20. Glossary

2.1.21. Index

2.1.22. Bibliography

2.1.23. Appendix

2.1.24. Figures

2.1.25. Tables

2.1.26. Glossary

2.1.27. Index

2.1.28. Bibliography

2.1.29. Appendix

2.1.30. Figures

2.1.31. Tables

2.1.32. Glossary

2.1.33. Index

2.1.34. Bibliography

2.1.35. Appendix

2.1.36. Figures

2.1.37. Tables

2.1.38. Glossary

2.1.39. Index

2.1.40. Bibliography

2.1.41. Appendix

2.1.42. Figures

2.1.43. Tables

2.1.44. Glossary

2.1.45. Index

2.1.46. Bibliography

2.1.47. Appendix

2.1.48. Figures

2.1.49. Tables

2.1.50. Glossary

2.1.51. Index

2.1.52. Bibliography

2.1.53. Appendix

2.1.54. Figures

2.1.55. Tables

2.1.56. Glossary

2.1.57. Index

2.1.58. Bibliography

2.1.59. Appendix

2.1.60. Figures

2.1.61. Tables

2.1.62. Glossary

2.1.63. Index

2.1.64. Bibliography

2.1.65. Appendix

2.1.66. Figures

2.1.67. Tables

2.1.68. Glossary

2.1.69. Index

2.1.70. Bibliography

2.1.71. Appendix

2.1.72. Figures

2.1.73. Tables

2.1.74. Glossary

2.1.75. Index

2.1.76. Bibliography

2.1.77. Appendix

2.1.78. Figures

2.1.79. Tables

2.1.80. Glossary

2.1.81. Index

2.1.82. Bibliography

2.1.83. Appendix

2.1.84. Figures

2.1.85. Tables

2.1.86. Glossary

2.1.87. Index

2.1.88. Bibliography

2.1.89. Appendix

2.1.90. Figures

2.1.91. Tables

2.1.92. Glossary

2.1.93. Index

2.1.94. Bibliography

2.1.95. Appendix

2.1.96. Figures

2.1.97. Tables

2.1.98. Glossary

2.1.99. Index

2.1.100. Bibliography

2.1.101. Appendix

2.1.102. Figures

2.1.103. Tables

2.1.104. Glossary

2.1.105. Index

2.1.106. Bibliography

2.1.107. Appendix

2.1.108. Figures

2.1.109. Tables

2.1.110. Glossary

2.1.111. Index

2.1.112. Bibliography

2.1.113. Appendix

2.1.114. Figures

2.1.115. Tables

2.1.116. Glossary

2.1.117. Index

2.1.118. Bibliography

2.1.119. Appendix

2.1.120. Figures

2.1.121. Tables

2.1.122. Glossary

2.1.123. Index

2.1.124. Bibliography

2.1.125. Appendix

2.1.126. Figures

2.1.127. Tables

2.1.128. Glossary

2.1.129. Index

2.1.130. Bibliography

2.1.131. Appendix

2.1.132. Figures

2.1.133. Tables

2.1.134. Glossary

2.1.135. Index

2.1.136. Bibliography

2.1.137. Appendix

2.1.138. Figures

2.1.139. Tables

2.1.140. Glossary

2.1.141. Index

2.1.142. Bibliography

2.1.143. Appendix

2.1.144. Figures

2.1.145. Tables

2.1.146. Glossary

2.1.147. Index

2.1.148. Bibliography

2.1.149. Appendix

2.1.150. Figures

2.1.151. Tables

2.1.152. Glossary

2.1.153. Index

2.1.154. Bibliography

2.1.155. Appendix

2.1.156. Figures

2.1.157. Tables

2.1.158. Glossary

2.1.159. Index

2.1.160. Bibliography

2.1.161. Appendix

2.1.162. Figures

2.1.163. Tables

2.1.164. Glossary

2.1.165. Index

2.1.166. Bibliography

2.1.167. Appendix

2.1.168. Figures

2.1.169. Tables

2.1.170. Glossary

2.1.171. Index

2.1.172. Bibliography

2.1.173. Appendix

2.1.174. Figures

2.1.175. Tables

2.1.176. Glossary

2.1.177. Index

2.1.178. Bibliography

2.1.179. Appendix

2.1.180. Figures

2.1.181. Tables

2.1.182. Glossary

2.1.183. Index

2.1.184. Bibliography

2.1.185. Appendix

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2.1.288. Figures

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[illegible]

Run	Sample	Time (h)	Temp (°C)	Pressure (atm)	Flow Rate (L/min)	Detector	Analysis
1	Sample A	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
2	Sample B	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
3	Sample C	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
4	Sample D	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
5	Sample E	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
6	Sample F	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
7	Sample G	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
8	Sample H	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
9	Sample I	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
10	Sample J	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
11	Sample K	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
12	Sample L	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
13	Sample M	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
14	Sample N	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
15	Sample O	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
16	Sample P	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
17	Sample Q	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
18	Sample R	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
19	Sample S	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)
20	Sample T	1.0	100	1.0	1.0	FTIR	FTIR (1000-4000 cm ⁻¹)

[illegible][illegible]

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Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population growth rate (%)	Urban population growth rate (%)	Urban population growth rate (1970-1980) (%)
1	1980	10.4	4.1	39.4	2.1	3.1	1.0
2	1980	10.4	4.1	39.4	2.1	3.1	1.0
3	1980	10.4	4.1	39.4	2.1	3.1	1.0
4	1980	10.4	4.1	39.4	2.1	3.1	1.0
5	1980	10.4	4.1	39.4	2.1	3.1	1.0
6	1980	10.4	4.1	39.4	2.1	3.1	1.0
7	1980	10.4	4.1	39.4	2.1	3.1	1.0
8	1980	10.4	4.1	39.4	2.1	3.1	1.0
9	1980	10.4	4.1	39.4	2.1	3.1	1.0
10	1980	10.4	4.1	39.4	2.1	3.1	1.0
11	1980	10.4	4.1	39.4	2.1	3.1	1.0
12	1980	10.4	4.1	39.4	2.1	3.1	1.0
13	1980	10.4	4.1	39.4	2.1	3.1	1.0
14	1980	10.4	4.1	39.4	2.1	3.1	1.0
15	1980	10.4	4.1	39.4	2.1	3.1	1.0
16	1980	10.4	4.1	39.4	2.1	3.1	1.0
17	1980	10.4	4.1	39.4	2.1	3.1	1.0
18	1980	10.4	4.1	39.4	2.1	3.1	1.0
19	1980	10.4	4.1	39.4	2.1	3.1	1.0
20	1980	10.4	4.1	39.4	2.1	3.1	1.0
21	1980	10.4	4.1	39.4	2.1	3.1	1.0
22	1980	10.4	4.1	39.4	2.1	3.1	1.0
23	1980	10.4	4.1	39.4	2.1	3.1	1.0
24	1980	10.4	4.1	39.4	2.1	3.1	1.0
25	1980	10.4	4.1	39.4	2.1	3.1	1.0
26	1980	10.4	4.1	39.4	2.1	3.1	1.0
27	1980	10.4	4.1	39.4	2.1	3.1	1.0
28	1980	10.4	4.1	39.4	2.1	3.1	1.0
29	1980	10.4	4.1	39.4	2.1	3.1	1.0
30	1980	10.4	4.1	39.4	2.1	3.1	1.0
31	1980	10.4	4.1	39.4	2.1	3.1	1.0
32	1980	10.4	4.1	39.4	2.1	3.1	1.0
33	1980	10.4	4.1	39.4	2.1	3.1	1.0
34	1980	10.4	4.1	39.4	2.1	3.1	1.0
35	1980	10.4	4.1	39.4	2.1	3.1	1.0
36	1980	10.4	4.1	39.4	2.1	3.1	1.0
37	1980	10.4	4.1	39.4	2.1	3.1	1.0
38	1980	10.4	4.1	39.4	2.1	3.1	1.0
39	1980	10.4	4.1	39.4	2.1	3.1	1.0
40	1980	10.4	4.1	39.4	2.1	3.1	1.0
41	1980	10.4	4.1	39.4	2.1	3.1	1.0
42	1980	10.4	4.1	39.4	2.1	3.1	1.0
43	1980	10.4	4.1	39.4	2.1	3.1	1.0
44	1980	10.4	4.1	39.4	2.1	3.1	1.0
45	1980	10.4	4.1	39.4	2.1	3.1	1.0
46	1980	10.4	4.1	39.4	2.1	3.1	1.0
47	1980	10.4	4.1	39.4	2.1	3.1	1.0
48	1980	10.4	4.1	39.4	2.1	3.1	1.0
49	1980	10.4	4.1	39.4	2.1	3.1	1.0
50	1980	10.4	4.1	39.4	2.1	3.1	1.0

PROTEIN	GENES	PRIMER NAME	PRIM	SEQ. AA
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PH EP74609 A2
 XX 26-JAN-2000.
 XX 24-JUN-1999: 99EP-039477.
 XX 24-JUN-1998: 98JP-0177680.
 PR 12-DEC-1998: 98JP-0299344.
 PR 22-DEC-1998: 98JP-0365023.
 XX (HAYB.) HAYASHIMURA SEIICHIRO KAKAKU.
 XX Nishida Y., Okura T., Tanimoto T., Kurimoto M.
 OR WPI: 2000-119241/11.
 XX
 PR New artificiality produced peptide for neutralizing biological activity
 PT of Interleukin 18, useful for treating and preventing immunopathoses,
 PI inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure: Page 27: 32pp; English.
 CC The present sequence is mouse monoclonal Interleukin-18. This can comprise
 CC a part or the whole of the variable region in anti-Interleukin-18
 CC antibody for neutralizing Interleukin-18. This is useful for treating
 CC and preventing immunopathoses, inflammatory disorders and autoimmune
 CC diseases which are caused by excessive immunoreaction. The protein has
 CC anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic,
 CC leukopoietic, anti-lytic, antipyretic and hepatoregulation improving
 CC activities.
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 XX Sequence: 157 AA:
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 Query Match 99.48: Score 806: DB 21: Length 157:
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 DB 1 HTHHHT 60
 QY 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 DB 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 QY 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 DB 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 QY 121 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 157
 DB 121 HTHHHT 157
 RESULT 12
 V53905 Y53905 standard, 157 AA.
 AC Y53905
 XX
 DT 13-MAR-2000 (first entry)
 DE Amino acid sequence of a protein that induces TCR gamma production
 XX
 KW Mouse interferon gamma production: TCR gamma, immunoregulatory agent, cell,
 KW adjuvant, immunoregulatory agent, antitumor agent, antitumor,
 KW TCR gamma production: TCR gamma, antitumor agent, antitumor,
 KW blood platelet enhancing agent, hepatitis, herpes syndrome, condyloma,
 KW AIDS, bacterial diseases, candidiasis, malaria, solid malignant tumor,
 KW renal cancer, mycosis, tumours, chronic granulomatous diseases,
 KW blood cell malignant tumor, adult T cell leukemia,
 KW chronic myelogenous leukemia, malignant leukemia, immune diseases,
 KW allergy, rheumatism.
 XX
 XX Mus sp.
 OS
 XX

PH EP74609 A2
 XX 26-JAN-2000.
 XX 24-JUN-1999: 99EP-039477.
 XX 24-JUN-1998: 98JP-0177680.
 PR 12-DEC-1998: 98JP-0299344.
 PR 22-DEC-1998: 98JP-0365023.
 XX (HAYB.) HAYASHIMURA SEIICHIRO KAKAKU.
 XX Nishida Y., Okura T., Tanimoto T., Kurimoto M.
 OR WPI: 2000-119241/11.
 XX
 PR New artificiality produced peptide for neutralizing biological activity
 PT of Interleukin 18, useful for treating and preventing immunopathoses,
 PI inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure: Page 27: 32pp; English.
 CC The present sequence represents a murine protein that induces Interleukin
 CC (ILN)-gamma production by immunocompetent cells. ILN-gamma is a
 CC protein which has antitumor, antitumor, antitumor, antitumor,
 CC and is produced by immunocompetent cells stimulated with antigens or
 CC mitogens. A probe derived from the cDNA of the present sequence was used
 CC to isolate the corresponding human protein from human liver cells. The
 CC protein of the invention is used to treat TCR gamma compatible diseases,
 CC and also have use as a antitumor agent, antitumor agent, antitumor
 CC agent, immunoregulatory agent and blood platelet enhancing agent.
 CC diseases which can be treated with the protein include viral diseases
 CC such as hepatitis, herpes syndrome, condyloma, and AIDS; bacterial
 CC diseases such as candidiasis and malaria; solid malignant tumors such
 CC as renal cancer, mycosis, tumours, and chronic granulomatous diseases;
 CC blood cell malignant tumor, adult T cell leukemia, chronic
 CC myelogenous leukemia, and malignant leukemia and immune diseases
 CC such as allergy and rheumatism.
 XX
 XX Sequence: 157 AA:
 SQ
 Query Match 99.48: Score 806: DB 21: Length 157:
 Best Local Similarity 99.48: Pred. No. 1,20-75:
 Matches 156: Conservative 0: Mismatches 1: Gaps 0:
 QY 1 MPEFHTAVFNTNGVFEKPEVFETMTTNGSASPCSTHTTPVSGEVEGIA 60
 DB 1 HTHHHT 60
 QY 1 HTHHHT 60
 DB 1 HTHHHT 60
 QY 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 DB 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 QY 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 DB 61 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 120
 QY 121 VTHVTEFHELTSEHETSEETETETETETETETETETETETETETETETET 157
 DB 121 HTHHHT 157
 RESULT 13
 W77090 W77090 standard, 157 AA.
 AC W77090
 XX
 DT 16-NOV-1998 (first entry)
 DE Amino acid sequence of a protein that induces TCR gamma production
 XX
 KW Mouse interferon gamma production: TCR gamma, immunoregulatory agent, cell,
 KW adjuvant, immunoregulatory agent, antitumor agent, antitumor,
 KW TCR gamma production: TCR gamma, antitumor agent, antitumor,
 KW blood platelet enhancing agent, hepatitis, herpes syndrome, condyloma,
 KW AIDS, bacterial diseases, candidiasis, malaria, solid malignant tumor,
 KW renal cancer, mycosis, tumours, chronic granulomatous diseases,
 KW blood cell malignant tumor, adult T cell leukemia,
 KW chronic myelogenous leukemia, malignant leukemia, immune diseases,
 KW allergy, rheumatism.
 XX
 XX Mus sp.
 OS
 XX

[illegible]

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01 08 9906 400 27
02 08 9906 400 27
03 08 9906 400 27
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98 08 9906 400 27
99 08 9906 400 27
100 08 9906 400 27

```


[illegible][illegible]

LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single

PLASMENI YPH: intercalated liquid
115 18 578 813-4

Only Match: 15, 98; Score 129; DB 4; Length 25

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

M protein - protein search, using sw model

Run on: May 11, 2001, 16:37:48 ; Search time 23.4 Seconds

(without alignments)
451,090 Million cell updates/sec

Title: US-09-030-061-7
Perfect score: 812
Sequence: 1: RGRMLPFAVIRNINQVY.....KRLIMKGVNITLRLGQ 155

Scoring table:
Gapop 10.0 ; Gapext 0.5

Searched: 198803 56481 6822994 1001448

Total number of hits satisfying chosen parameters: 198601

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: PIR_57*
2: PIR1*
3: PIR2*
4: PIR3*
5: PIR4*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length (B)	ID	Description
1	812	100.0	564026	cytokine 101F mouse
2	810.5	100.3	A64070	endothelidase 1a (hypothetical prote
3	81	10.3	221327	hypothetical prote
4	81	10.0	JN0724	interleukin 1 beta
5	80.5	9.9	651636	cyt2. Interleukin 1
6	80.5	9.9	1039	hypothetical prote
7	80	9.9	1196	hypothetical prote
8	79.5	9.8	1396	hypothetical prote
9	79.5	9.8	1472	hypothetical prote
10	79.5	9.8	2672	hypothetical prote
11	79	9.7	521401	interleukin 1 beta
12	78.5	9.7	270	interleukin 1 alpha
13	78.5	9.7	698	hypothetical prote
14	78.5	9.7	734	hypothetical prote
15	78.5	9.7	1294	hypothetical prote
16	78	9.6	1146	hypothetical prote
17	78	9.6	1217	hypothetical prote
18	77.5	9.5	270	hypothetical prote
19	77.5	9.5	439	hypothetical prote
20	77	9.5	439	hypothetical prote
21	76.5	9.4	366	hypothetical prote
22	76.5	9.4	665	hypothetical prote
23	76.5	9.4	665	hypothetical prote
24	76.5	9.4	666	hypothetical prote
25	76.5	9.4	1146	hypothetical prote
26	76.5	9.4	1146	hypothetical prote
27	76	9.4	592	hypothetical prote
28	76	9.4	592	hypothetical prote
29	76	9.4	593	hypothetical prote

40	75.5	9.3	547	hypothetical protein
41	75.5	9.3	547	hypothetical protein
42	75	9.2	260	interleukin 1 beta
43	75	9.2	35	hypothetical prote
44	75	9.2	324	hypothetical prote
45	75	9.2	62	hypothetical prote
46	74.5	9.2	66	hypothetical prote
47	74.5	9.2	706	hypothetical prote
48	74.5	9.2	2077	hypothetical prote
49	74.5	9.2	2077	hypothetical prote
50	74	9.1	254	hypothetical prote
51	74	9.1	259	hypothetical prote
52	74	9.1	254	hypothetical prote
53	74	9.1	259	hypothetical prote
54	74	9.1	259	hypothetical prote
55	74	9.1	259	hypothetical prote

ALIGNMENTS

RESULT 1

Seq226 mouse

Cytoprote: Mus musculus (house mouse)

Query: 10 Apr 1996 #sequence revision by Apr 1996 #next change 20 Jan 2000

Cytoprote: Seq226

Protein: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Match: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

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Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Alignment: 101F (Interleukin 1 beta) (Kabat, E. A. et al., 1996)

Annotation: Uncloned form containing entire mature form (15-270) a form containing 141-270
 Comments: Produced by a different coding frame, the 11 protein, identical to the mature form of the

Comments: The protein is involved in the inflammatory response, being involved in the

Comments: This protein has a predicted molecular weight of 100 kDa and is a member of the

Comments: This protein has a predicted molecular weight of 100 kDa and is a member of the

Comments: This protein has a predicted molecular weight of 100 kDa and is a member of the

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Comments: This protein has a predicted molecular weight of 100 kDa and is a member of the

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Query Match: 9.7%, Score 79.6, DB: 1, Length 608

Best local similarity: 22.4%, Prod. No. 27

Matches: 20, Conservation: 24, Mismatches: 14, Indels: 17, Gaps: 7

Database version 4.5
Copyright (c) 1993 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2001, 16:49:07 : Search time 13.78 seconds

(without attachments)
490,284 Million cell updates/sec

Hit list:
Perfect score: 81.2

Sequence: 1 REFLECTTAVLHRTNRYV.....KRIKREKSVMTTILHDS 157

Scoring table:

BLASTSUM62

Gapop 10.0, Gapext 0.5

Searched: 9435 seqs, 4425486 residues

Total number of hits satisfying chosen parameters: 9435

Minimum hit seq length: 7

Maximum hit seq length: 206000000

Post-processing: Minimum March 08

Maximum March 1008

Listing first 45 summaries

Database: SwissProt_49*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query March	Length	Hit ID	Description
1	81.2	20.0	192	1118_MOUSE	F70360 Mus musc
2	74.25	91.4	194	1118_RAT	P97536 Rattus nor
3	53.7	66.1	193	1118_HORSE	Q9XSP7 Equus cabal
4	52.0	64.0	193	1118_HUMAN	Q14176 Homo sapien
5	51.6	61.5	193	1118_CANINA	Q9XSP7 Canis fami
6	51.5	61.4	192	1118_PIG	Q19073 Sus scrofa
7	83.5	10.3	803	1118_MOUSE	P43864 Haemophilus
8	81	10.0	267	1118_PIG	P22989 Sus scrofa
9	80.5	9.9	526	1118_MOUSE	Q90382 Saccharomy
10	80	9.9	1196	1118_MOUSE	P45021 Canis fami
11	79.5	9.8	167	1118_MOUSE	Q78273 Canis fami
12	79	9.7	266	1118_MOUSE	P09428 Bos taurus
13	78.5	9.7	270	1118_MOUSE	P01582 Mus musc
14	78.5	9.7	698	1118_MOUSE	P08293 Canis fami
15	77.5	9.5	270	1118_MOUSE	P18430 Sus scrofa
16	77.5	9.5	439	1118_MOUSE	Q78221 Canis fami
17	77	9.5	885	1118_MOUSE	Q90382 Saccharomy
18	76.5	9.4	621	1118_MOUSE	P56116 Mus musc
19	76.5	9.4	695	1118_MOUSE	P45306 Haemophilus
20	75	9.2	266	1118_MOUSE	P21621 Canis fami
21	75	9.2	269	1118_MOUSE	P19000 Canis fami
22	75	9.2	269	1118_MOUSE	P51403 Canis fami
23	75	9.2	621	1118_MOUSE	Q92002 Canis fami
24	74.5	9.2	706	1118_MOUSE	P56116 Mus musc
25	74	9.1	268	1118_MOUSE	P29182 Canis fami
26	74	9.1	269	1118_MOUSE	P01584 Canis fami
27	74	9.1	624	1118_MOUSE	Q10156 Canis fami
28	74	9.1	624	1118_MOUSE	Q10156 Canis fami
29	74	9.1	624	1118_MOUSE	Q10156 Canis fami
30	74	9.1	624	1118_MOUSE	Q10156 Canis fami
31	74	9.1	624	1118_MOUSE	Q10156 Canis fami
32	74	9.1	624	1118_MOUSE	Q10156 Canis fami
33	74	9.1	624	1118_MOUSE	Q10156 Canis fami
34	74	9.1	624	1118_MOUSE	Q10156 Canis fami

44	74	9.0	542	1118_MOUSE	P44973 Haemophilus
45	72.5	8.9	589	1118_MOUSE	P48654 Haemophilus
46	72.5	8.9	589	1118_MOUSE	P48654 Haemophilus
47	72.5	8.9	589	1118_MOUSE	P48654 Haemophilus
48	72	8.9	511	1118_MOUSE	P48654 Haemophilus
49	72	8.9	796	1118_MOUSE	P48654 Haemophilus
40	72	8.9	796	1118_MOUSE	P48654 Haemophilus
41	71.5	8.8	794	1118_MOUSE	P48654 Haemophilus
42	71.5	8.8	794	1118_MOUSE	P48654 Haemophilus
43	71	8.7	266	1118_MOUSE	P48654 Haemophilus
44	71	8.7	266	1118_MOUSE	P48654 Haemophilus
45	71	8.7	266	1118_MOUSE	P48654 Haemophilus

ALTERNATIVES

1	1118_MOUSE	STANDARD	PREL	192 AA.
2	1118_MOUSE	STANDARD	PREL	192 AA.
3	1118_MOUSE	STANDARD	PREL	192 AA.
4	1118_MOUSE	STANDARD	PREL	192 AA.
5	1118_MOUSE	STANDARD	PREL	192 AA.
6	1118_MOUSE	STANDARD	PREL	192 AA.
7	1118_MOUSE	STANDARD	PREL	192 AA.
8	1118_MOUSE	STANDARD	PREL	192 AA.
9	1118_MOUSE	STANDARD	PREL	192 AA.
10	1118_MOUSE	STANDARD	PREL	192 AA.
11	1118_MOUSE	STANDARD	PREL	192 AA.
12	1118_MOUSE	STANDARD	PREL	192 AA.
13	1118_MOUSE	STANDARD	PREL	192 AA.
14	1118_MOUSE	STANDARD	PREL	192 AA.
15	1118_MOUSE	STANDARD	PREL	192 AA.
16	1118_MOUSE	STANDARD	PREL	192 AA.
17	1118_MOUSE	STANDARD	PREL	192 AA.
18	1118_MOUSE	STANDARD	PREL	192 AA.
19	1118_MOUSE	STANDARD	PREL	192 AA.
20	1118_MOUSE	STANDARD	PREL	192 AA.
21	1118_MOUSE	STANDARD	PREL	192 AA.
22	1118_MOUSE	STANDARD	PREL	192 AA.
23	1118_MOUSE	STANDARD	PREL	192 AA.
24	1118_MOUSE	STANDARD	PREL	192 AA.
25	1118_MOUSE	STANDARD	PREL	192 AA.
26	1118_MOUSE	STANDARD	PREL	192 AA.
27	1118_MOUSE	STANDARD	PREL	192 AA.
28	1118_MOUSE	STANDARD	PREL	192 AA.
29	1118_MOUSE	STANDARD	PREL	192 AA.
30	1118_MOUSE	STANDARD	PREL	192 AA.
31	1118_MOUSE	STANDARD	PREL	192 AA.
32	1118_MOUSE	STANDARD	PREL	192 AA.
33	1118_MOUSE	STANDARD	PREL	192 AA.
34	1118_MOUSE	STANDARD	PREL	192 AA.
35	1118_MOUSE	STANDARD	PREL	192 AA.
36	1118_MOUSE	STANDARD	PREL	192 AA.
37	1118_MOUSE	STANDARD	PREL	192 AA.
38	1118_MOUSE	STANDARD	PREL	192 AA.
39	1118_MOUSE	STANDARD	PREL	192 AA.
40	1118_MOUSE	STANDARD	PREL	192 AA.
41	1118_MOUSE	STANDARD	PREL	192 AA.
42	1118_MOUSE	STANDARD	PREL	192 AA.
43	1118_MOUSE	STANDARD	PREL	192 AA.
44	1118_MOUSE	STANDARD	PREL	192 AA.
45	1118_MOUSE	STANDARD	PREL	192 AA.

[illegible]

RESULT 4
FILE: pmph
ID IL16_HUMAN STANDARD: PR1: 193 AA.
AC 014116: 075598.
DI 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN 16 PRESENT IN CD16+ AND CD16- B CELLS
DE (IL16 GAMMA INDUCING FACTOR) (INTERLEUKIN 1 GAMMA) (IL-1 GAMMA).
GN IL16 OR IL16F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI-TaxID: 9606.
PE 111.
RN 1.
RP SPORADIC FROM N.A.
RC TISSUE: Liver.
RX MEDLINE 96-21746; PubMed-8665798;
RA Ushio S., Nakata M., Ikeda M., Ishii K., Nakada T., Akita K.,
RA Tando T., Katsuki K., Miyajima M., Fujii M., Torigoe K., Miyajima F.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.,
RI Cloning of the cDNA for human (IL16 gamma inducing factor) expressed
in Escherichia coli, and studies on the biological activities of the
protein. J. Biol. Chem. 271:15642-15647 (1996).
RI 2. Immanuel. 1564274-4279(1996).
RN 1.
RP SPORADIC FROM N.A.
RC TISSUE: Peripheral blood.
RA Conti R., Kim S.J., Hui C., Chan H.S., Job F.H.,
RI Cloning and sequencing of the cDNA for precursor hIL-18. J.
submitted (JUL-1998) to the EMBL/GenBank/Trna databases.
RN 1.
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE: Peripheral blood.
RA Conti R., Kim S.J., Hui C., Chan H.S., Job F.H.,
RI Submitted (FEB-1997) to the EMBL/GenBank/Trna databases.
RN 1.
RP FUNCTION: ARGUMENTS NATIONAL KILLER CELL ACTIVITY IN SPLENEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC or send an email to license@sb-sib.ch).
DE EMBL: 049950; BAA08706.1;
DE EMBL: AF077611; AAC27787.1;
DE EMBL: D90434; AAB50010.1;
DE MIM: 600643;
KM Cytokine.
FT PROPEP 1 36 PE SIMILARITY
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 56 66 F-1 (IN PRO. 2)
FT CONFLICT 86 86 S-2 R (IN REF. 2).
FT CONFLICT 191 191 N-2 S (IN REF. 2).
SU SEQUENCE 193 AA: 27325 MW: 32402.2023738055 CRRGSA;
Query Match 64.0% Score 5201 DB 1: Length 1933
Best Local Similarity 65.6% Prod. No. 3,96-402
Matches 101: Conservative 27: Mismatches 24: Indels 2: Gaps 2:
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 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2421 2422 2423 2

[illegible]

Mammalia; eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI: 6441475; PubMed: 6441475; PubMed: 6441475;
 RA: Huchler M., Liu G., Smith D.M., Murtanah M.P., Mollot T.W.;
 RT: Interleukin-1 beta;
 RT: Interleukin-1 beta;
 RT: Gene 1291255-289(1992).
 CC: -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC: THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC: MATURATION & PROLIFERATION, & T-CELL GROWTH FACTOR ACTIVITY.
 CC: IL-1 PEPTIDES ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC: IDENTIFIED AS ENDOTOXIN PYROGENS, AND ARE REPORTED TO STIMULATE
 CC: THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC: -1- SUBUNIT: MONOMER.
 CC: -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC: AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC: MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC: PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY LAMINAR FLUX
 CC: OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC: SECRETORY PROTEINS.
 CC: -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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 CC: or send an email to license@ebi.ac.uk).
 CC: EMBL: M66725; AAC02594.1;
 CC: DR: PIR: J00724; J00724;
 CC: DR: HSSP: P01584; 181H;
 CC: DR: InterPro: IPR000975;
 CC: DR: InterPro: IPR002148;
 CC: DR: Pfam: PF00440; InterPro: IPR000975;
 CC: DR: PRINTS: PR00242; IL1HG;
 CC: DR: PRINTS: PR00244; INTERLEUKIN1;
 CC: DR: PROSITE: PS00253; INTERLEUKIN1;
 CC: KW: cytokine; interleukin; interleukin; interleukin; interleukin; interleukin;
 CC: FT: PROPEP 1 114 BY SIMILARITY;
 CC: FT: CHAIN 115 267 INTERLEUKIN-1 BETA;
 CC: SEQUENCE 267 AA; 29404 MW; 706928784B96CF DE547;
 Query Match 10.0%; Score 81; DB 1; Length 267;
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 Matches 24; Conserved 22; Mismatches 41; Indels 12; Gaps 0;
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 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 160 KVENNNKIPVLCIG-KNLYLSYMNNTITLCEHLEPPRYKR--DMKRRIVY 216
 CC: 102 KVENNNKIPVLCIG-KNLYLSYMNNTITLCEHLEPPRYKR--DMKRRIVY 216
 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 217 KVEI KNEVPSALVPMVYISQAE 242
 RESULT 9
 ZAWA_YEAST STANDARD PR1 526 AA
 AT 600762
 DT 01-APR-1993 (Ref. 25, Created)
 DT 01-OCT-1996 (Ref. 34, Last sequence update)
 DT 15-JUL-1999 (Ref. 38, Last annotation update)
 DE PROTEIN PROPHASIN PF2A FROM THE YEAST SUPPLEMENT 5 (1995) (CELL DIVISION
 DE CONTROL PROTEIN 55).
 GN CDK5; OR YH1906; GI 1345
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

NCBI: 6441475; PubMed: 6441475; PubMed: 6441475;
 RA: Huchler M., Liu G., Smith D.M., Murtanah M.P., Mollot T.W.;
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 CC: IL-1 PEPTIDES ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
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 CC: THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC: -1- SUBUNIT: MONOMER.
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 CC: PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY LAMINAR FLUX
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 CC: -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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 CC: or send an email to license@ebi.ac.uk).
 CC: EMBL: M66725; AAC02594.1;
 CC: DR: PIR: J00724; J00724;
 CC: DR: HSSP: P01584; 181H;
 CC: DR: InterPro: IPR000975;
 CC: DR: InterPro: IPR002148;
 CC: DR: Pfam: PF00440; InterPro: IPR000975;
 CC: DR: PRINTS: PR00242; IL1HG;
 CC: DR: PRINTS: PR00244; INTERLEUKIN1;
 CC: DR: PROSITE: PS00253; INTERLEUKIN1;
 CC: KW: cytokine; interleukin; interleukin; interleukin; interleukin; interleukin;
 CC: FT: PROPEP 1 114 BY SIMILARITY;
 CC: FT: CHAIN 115 267 INTERLEUKIN-1 BETA;
 CC: SEQUENCE 267 AA; 29404 MW; 706928784B96CF DE547;
 Query Match 10.0%; Score 80.5; DB 1; Length 526;
 Post Local Similarity 26.0%; Ident. No. 5.2;
 Matches 66; Conserved 49; Mismatches 96; Indels 24; Gaps 7;
 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 160 KVENNNKIPVLCIG-KNLYLSYMNNTITLCEHLEPPRYKR--DMKRRIVY 216
 CC: 102 KVENNNKIPVLCIG-KNLYLSYMNNTITLCEHLEPPRYKR--DMKRRIVY 216
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 CC: 1- YHFEIETLAVLAVLSEK...LKKK...LELEH...PERH...LLEIT...161
 CC: 217 KVEI KNEVPSALVPMVYISQAE 242
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 ZAWA_YEAST STANDARD PR1 526 AA
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 DT 01-OCT-1996 (Ref. 34, Last sequence update)
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 DE PROTEIN PROPHASIN PF2A FROM THE YEAST SUPPLEMENT 5 (1995) (CELL DIVISION
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